REMARKS

Status of the claims

Claims 1, 4, 18, and 24 have been amended. New claims 33-41 have been added.

Claims 1, 4, 18, and 24 have been amended to clarify that that stringent conditions comprise hybridization at 37°C in 50% formamide, 1 M NaCl, and 1% SDS and a wash in 0.1X SSC at 60°C. Support for the amendments to the claims can be found in the specification, particularly at page 19, lines 20-23.

New claims 33-41 have been added. Support for the new claims can be found in original claims 1, 4, and 11 and in the specification, particularly on page 15, lines 9-14.

No new matter has been added by way of amendment of the claims or by the addition of the new claims.

Claims 1-18, 20-24, and 33-41 are pending.

Reexamination and reconsideration of the application as amended are respectfully requested.

The Rejections of the Claims Under 35 U.S.C. § 112, First Paragraph, Should Be Withdrawn

Claims 1-18 and 20-24 have been rejected under 35 U.S.C. § 112, first paragraph. Claims 1, 4, 18, and 24 have been amended. New claims 33-41 have been added. This rejection is respectfully traversed and should not be applied to the newly submitted claims.

Claims 1-18 and 20-24 were rejected under 35 U.S.C. § 112, first paragraph, for containing subject matter which was not described in the specification in a such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the invention. The Office Action indicates that Applicants do not describe other nucleotide molecules encoding a non-mutant P-glycoprotein that controls plant growth other than that of SEQ ID NO:7 or 8, or a nucleotide molecule that encodes the amino acid sequence of SEQ ID NO: 9. The Office Action asserts that such a description would also be

required to envision a nucleic acid that would bind under the claimed stringency conditions. The Office Action indicates that Applicants have only described a single nucleotide molecule that encodes the P-glycoprotein of SEQ ID NO: 9 because SEQ ID NO: 7 is the genomic sequence for the cDNA exemplified in SEQ ID NO: 8.

The Office Action indicates a biomolecule sequence described only by a functional characteristic is normally insufficient for written description purposes even when accompanied by a method of obtaining the claimed sequence. The Office Action cites in support of this position MPEP § 2160, which states that the claimed invention as a whole may not be adequately described where an invention is described solely in terms of a method of its making coupled with its function in absence of a correlation between the structure of the invention and its function. The pending claims meet the standard set forth by the Examiner. The claims recite that the nucleotide molecules comprise a structural characteristic (at least 80% sequence identity to SEQ ID NO: 7 and/or SEQ ID NO: 8) and a functional characteristic (the nucleotide molecule encodes a P-glycoprotein that controls plant growth or said nucleotide molecule is complementary to a nucleotide sequence that encodes said P-glycoprotein).

The Office Action concludes that the claimed genus of nucleotide molecules that encode P-glycoproteins that function to control plant growth is not adequately described because Applicants have not described what structural characteristics within the 80% limitation are correlated with the function of the claimed nucleotide molecule. The Examiner is reminded that the first paragraph of §112 provides, in pertinent part, that "[t]he specification shall contain a written description of the invention." The Federal Circuit, in discussing the standard for determining compliance with the written description requirement, has provided that "[t]he test for sufficiency of support . . . is whether the disclosure of the application reasonably conveys to the artisan that the inventor had possession at that time of the later claimed subject matter. *Vas-Cath Inc. v. Mahurkar*, 19 U.S.P.Q.2d 1111, 1116 (Fed. Cir. 1991) (citing *Ralston Purina Co. v. Far-Mar-Co, Inc.*, 227 U.S.P.Q. 177, 179 (Fed.Cir.1985) (quoting *In re Kaslow*, 217 U.S.P.Q 1089, 1096 (Fed.Cir.1983))).

The Office Action states that "Applicant's arguments . . . have been fully considered but they are not persuasive" and maintains the grounds for rejection set forth in the previous Office Action. Paper No. 14, p. 3. In maintaining these grounds for rejection, the Examiner disregards not only Applicants' arguments but also the case law cited in those arguments. Applicants respectfully submit that the Examiner is applying an extraordinarily high standard of written description to the present claims, a standard that is not properly based on case law or on the statute.

Applicants respectfully maintain that the present claims and specification meet the 35 U.S.C. §112 written description requirement as clarified by the Federal Circuit in *Regents of the University of California v. Eli Lilly and Co.*, 43 U.S.P.Q.2d 1398 (Fed. Cir. 1997) and *Amgen Inc. v. Chugai Pharmaceutical Co.*, 18 U.S.P.Q.2d 1016 (Fed. Cir. 1991). As discussed in their previous communication to the Office, Applicants have provided exemplary sequences of the invention and have thus provided a structural definition of the sequences of the invention. Applicants have also provided assays by which those of skill in the art can readily assess whether a nucleic acid molecule meeting the nucleotide sequence element of the claims also meets the functional limitation element of the claims. This is what *Lilly* requires. 43 U.S.P.Q.2d at 1406. Thus, Applicants have also conceived the sequences of the invention as articulated in *Amgen*; that is, Applicants are able "to envision the detailed constitution of a gene so as to distinguish it from other materials, as well as a method for obtaining it." 18 U.S.P.Q.2d at 1021.

The claimed genus in the present application is defined in the specification by the functional properties (*i.e.*, encode P-glycoproteins that function to control plant growth) and the structural properties (*i.e.*, sequence identity with disclosed sequences) shared by the encompassed species. This description is sufficient to distinguish the claimed genus from other materials. Accordingly, the disclosure of many species within the claimed genus is not required.

In view of the discussion above, it is apparent that those of ordinary skill in the art would not consider the written description inadequate given the breadth of the previously pending claims. Accordingly, the claims met the written description requirement and should not have

been rejected. In any event, the Examiner is respectfully requested to enter the above amendments for purposes of furthering prosecution.

Claims 1-18 and 20-24 have been rejected under 35 U.S.C. § 112, first paragraph, because the specification while being enabling for a method for modifying growth of a sorghum plant comprising transforming said sorghum plant with a construct comprising either a nucleotide molecule having the nucleotide sequence of SEQ ID NO: 7 or 8 in either the sense of antisense configuration, does not reasonably provide enablement for a method of modifying growth of any organism. This rejection is respectfully traversed.

With regard to enablement, Applicants discussed in their previous response (dated August 21, 2002) that that those of ordinary skill in the art, provided with the guidance in the present specification, could readily make and use the invention. Applicants noted that, provided with the exemplary disclosed nucleotide sequences of SEQ ID NO: 7 and 8, those of ordinary skill in the art can readily determine the nucleic acid sequence of a nucleic acid molecule as well as the percent identity between any two sequences. Furthermore, as disclosed in the specification, routine assays are known in the art that can be used by those of ordinary skill in the art to readily determine whether a nucleotide sequence encodes a P-glycoprotein that controls plant growth. Thus, one of ordinary skill in the art can readily determine whether a particular nucleotide sequence encodes a P-glycoprotein that controls the growth of any plant. Accordingly, a rational scheme for making and using the claimed nucleotide sequence is provided, and one of ordinary skill in the art can readily determine whether a particular sequence meets the nucleotide sequence element of the claims and the functional limitation element of the claims. Applicants submit that for this reason, the rejected claims meet the requirements of 35 U.S.C. § 112, first paragraph.

Applicants note that decisions in cases involving molecular biology also support Applicants' position. In *Hybritech Inc. v. Monoclonal Antibodies, Inc.*, 231 U.S.P.Q. 81 (Fed. Cir. 1986), the United States Court of Appeals for the Federal Circuit (hereinafter "Federal Circuit") held that claims were enabled where the necessary method for producing monoclonal

antibodies was well known in the art prior to the filing date. Similarly, in the recent case *Ajinomoto Co. v. Archer-Daniels-Midland Co.*, 56 U.S.P.Q.2d 1332 (Fed. Cir. 2000), *cert. denied* 532 U.S. 1019 (May 14, 2001), the Federal Circuit found claims to be enabled where steps of the claimed method required the use of molecular biology techniques and a test for functionality. In finding that the claims were enabled, the Federal Circuit noted that "all of the methods needed to practice the invention were well known to those skilled in the art" and that "the process used conventional and well-known genetic engineering techniques." *Id.* at 1337. In the instant application, while the exemplary sequences disclosed are novel, the methods for determining related sequences within the scope of the claims and for determining whether a sequence encodes a P-glycoprotein that functions to control the growth of a plant are known in the art. Accordingly, the rejected claims meet the statutory enablement requirement and this rejection should be withdrawn.

Applicants note that in their previous communication to the Office, Applicants discussed the appropriate standard for determining whether undue experimentation would be required to make and use an invention, which was articulated in *In re Wands*, 8 U.S.P.Q.2d 1400 (Fed. Cir. 1988). Those of ordinary skill in the art recognize that it is now customary in the art to make, by methods such as, for example, DNA shuffling, and assay a number of sequences for a desired function in order to achieve the best results. *See, e.g.*, Minshull and Stemmer (1999) *Current Opinion in Chemical Biology* 3:284-290, entitled "Protein Evolution by Molecular Breeding"; and Christians *et al.* (1999) *Nature Biotechnology* 17: 259-264, entitled "Directed evolution of thymidine kinase for AZT phosphorylation using DNA family shuffling." These and other similar publications in the art demonstrate that experiments comprising the generation and testing of a very large number of variant sequences for a desired function are now considered routine in the art. Methods for transforming a wide variety of plants, including both monocots and dicots, to express a nucleotide molecule of interest are considered routine to those of ordinary skill in the art. Furthermore, methods for determining the effects of the expression of such a nucleotide molecule on the growth a plant — such as, for example, measuring shoot height and shoot growth rate — are also routine. Because such experiments are routine, they

would not be considered "undue experimentation" under *In re Wands*. Accordingly, Applicants submit that the practice of the claimed methods does not require undue experimentation.

The Office Action states that "Applicant's arguments . . . have been fully considered but they are not persuasive" and maintains the grounds for rejection set forth in the previous Office Action and sets forth issues that affect the additionally rejected claims. Paper No. 14, p. 5. In maintaining the grounds for rejection set forth in the previous Office Action, the Examiner disregards not only Applicants' arguments but also the case law cited in those arguments. Applicants respectfully submit that the Examiner is applying an extraordinarily high standard of enablement to the present claims, a standard that is not properly based on case law or on the statute as will be discussed more fully below.

The Office Action also indicates that the rejection for lack of enablement has been modified to include claims 1-17 and 24 because Applicant has provided only limited guidance for those critical features of a P-glycoprotein that are required to modify the growth of a transformed plant as claimed. The Office Action cites the teachings of Bowie *et al.* ((1990) *Science* 247:1306-1310), Lazar *et al.* ((1988) *Mol. Cell. Biol.* 8:1247-1252), Broun *et al.* ((1998) *Science* 282:1315-1317), Hill *et al.* ((1998) *Biochem. Biophys. Res. Comm.* 244:573-577), and Fourgoux-Nicol *et al.* ((1999) *Plant Mol. Biol.* 40:857-872) in support of this position.

The Office Action asserts that the art teaches that it cannot be predicted by one of skill in the art that nucleic acids that are 80% identical will encode a protein with the same activity as that exemplified by SEQ ID NO: 9. In support of this assertion, the Office Action cites Bowie *et al.* as teaching that the positions within a protein's sequence where amino acid substitutions can be made with a reasonable expectation of maintaining function are limited and that certain positions are critical to the three-dimensional structure/function relationship and can tolerate only conservative substitutions or none at all. The Office Action cites Lazar *et al.* and Broun *et al.* as teaching that one or a few amino acid substitutions could dramatically affect the biological activity and the structure-function characteristics of a protein and that Lazar *et al.* and Hill *et al.* teach that making conservative substitutions does not produce predictable results. Curiously,

however, the Office Action fails to mention that one of the cited references, Bowie *et al.*, also teaches that "*proteins are surprisingly tolerant of amino acid substitutions*," and further that "in studying the effects of 1500 single amino acid substitutions at 142 positions in *lac* repressor, Miller and co-workers found that about one-half of all substitutions were phenotypically silent" (p. 1306, right col. (emphasis added)).

The Office Action asserts that, as to the limitation of a nucleotide sequence that hybridizes under the claimed stringent conditions, the art teaches isolating DNA fragments using stringent hybridization conditions does not always select for DNA fragments whose contiguous nucleotide sequence is the same or nearly the same as the probe or sequence of interest. The Office Action cites the teachings of Fourgoux-Nicol *et al.* in support of this assertion. The Office Action indicates that this reference teaches "the probe and isolated DNA fragment exhibited a number of sequence differences comprising a 99bp insertion within the probe and a single nucleotide gap, while the DNA fragment contained 2 single nucleotide gaps and together the fragments contained 27 nucleotide mismatches." Paper No. 14, p. 7. The Office Action then asserts that "[t]aking into account the insertions, gaps and mismatches, the longest stretch of contiguous nucleotides to which the probe could hybridize consisted of 93bp of DNA (page 862, Figure 2)," and that "the isolated fragment exhibits less than 50% sequence identity with probe." Paper No. 14, pp. 7-8.

The Office Action, however, is misleading with respect to its description of the teachings of Fourgoux-Nicol *et al.* because this reference teaches on page 863 that "[a]lignment of their nucleotide sequences shows that the M3 cDNA differs essentially from M3.21 by an insertion of 99 bp constituted by three repeats of the same motif." The M3 cDNA and M3.21 are the probe and the isolated DNA, respectively, as referred to in the Office Action. Furthermore, the Office Action fails to mention that over an 87 base contiguous stretch, the probe and the isolated DNA are identical at 85 of those 87 bases without any gaps (page 862, Figure 2). Over this stretch, the nucleotide sequence identity of the two DNA sequences is 97.7%. Similarly, the Office Action fails to mention that over a 245 bp region of the probe, the isolated DNA is identical at 217 of those 245 positions (with each of three single base pair gaps counted as a mismatch). Over this

stretch, the nucleotide sequence identity of the two DNA sequences is 88.6%. Finally, it would appear that to arrive at a figure of less than 50% sequence identity between the isolated fragment and the probe, the Examiner likely included nucleotides within the 99 base gap as well as sequences 5' and/or 3' to the overlapping regions of the two DNA sequences. Those of ordinary skill in the art will most certainly recognize that such a calculation of percent sequence identity is not indicative as to whether two partially complementary DNA strands would hybridize under stringent conditions. Thus, the Fourgoux-Nicol *et al.* reference fails to support the position of the Office Action that the art teaches isolating DNA fragments using stringent hybridization conditions does not always select for DNA fragments whose contiguous nucleotide sequence is the same or nearly the same as the probe or sequence of interest.

In view of the discussion above, it is apparent that those of ordinary skill in the art would not consider the amount of experimentation to determine whether a given nucleotide molecule fell within these claims to be undue. Accordingly, the claims met the statutory enablement requirement and should not have been rejected. In any event, the Examiner is respectfully requested to enter the above amendments for purposes of furthering prosecution.

In view of these amendments and remarks, Applicants respectfully assert that the present specification does meet the statutory enablement and written description requirements. Accordingly, Applicants respectfully request reconsideration and withdrawal of the rejections of the claims under 35 U.S.C. §112, and submit that these rejections should not be applied to the new claims.

The Rejection of the Claims Under 35 U.S.C. § 102(b) Should Be Withdrawn

Claims 1-6, 9, 11-13, 16, 18, 20, 21, and 24 have been rejected under 35 U.S.C. § 102(b) as being anticipated by Sidler *et al.* ((1998) *Plant Cell* 10:15623-1636). Claims 1, 4, 18, and 24 have been amended. New claims 33-41 have been added. This rejection is respectfully traversed and should not be applied to the newly submitted claims.

The Office Action indicates that the Sidler *et al.* reference discloses complementary sequences of said isolated nucleotide molecule, an expression cassette comprising said sense and antisense nucleotide molecules operably linked to a constitutive promoter, and plants transformed with said cassette. The Office Action furthers indicates that the Sidler *et al.* reference discloses: that the native promoter of the *AtPGP1* gene is a tissue-preferred promoter; that the isolated nucleotide molecule encodes a P-glycoprotein that functions to control the growth of an organism; a method of modifying the growth of a plant comprising transforming a plant with an antisense construct operably linked to a constitutive promoter that produces an antisense transcript that modifies the growth of a plant, specifically *Arabidopsis thaliana*; and a method of modifying the growth of a plant comprising transforming a plant with a sense construct, leading to the production of longer roots due to overexpression of the gene product. The Office Action asserts that the transformed monocot plants at claims 7, 8, 14, 15, 22, and 23 would have been considered functional equivalents of the *Arabidopsis* plant of Sidler *et al.* and concludes that the Sidler *et al.* reference has previously disclosed all of the claim limitations.

The Office Action asserts that the Sidler *et al.* reference discloses an isolated nucleotide molecule that would hybridize under the claimed stringency conditions to SEQ ID NO: 7 or 8. The Examiner notes that the there is no recitation of washing time(s) in the instant claims, and the recited wash conditions are only of low to moderate stringency. The Office Action cites the Fourgoux-Nicol *et al.* reference in support of this position.

Applicants respectfully disagree with the position of the Office Action because, under the recited stringency conditions, the isolated nucleotide molecule disclosed in the Sidler *et al.* reference would not hydridize to the nucleotide sequence set forth in either SEQ ID NO: 7 or 8. As discussed above, the Fourgoux-Nicol *et al.* reference fails to support the position of the Office Action that the art teaches isolating DNA fragments using stringent hybridization conditions does not always select for DNA fragments whose contiguous nucleotide sequence is the same or nearly the same as the probe or sequence of interest. However, in the interest of furthering prosecution of the application, Applicants have amended claims 1, 4, 18, and 24 to recite that stringent conditions comprise hybridization at 37°C in 50% formamide, 1 M NaCl,

and 1% SDS and a wash in 0.1X SSC at 60°C. Applicants submit that the isolated nucleotide molecule disclosed in the the Sidler *et al.* reference would not hydridize to the nucleotide sequence set forth in either SEQ ID NO: 7 or 8 under the hybridization conditions recited in the amended claims, and therefore, the nucleotide molecules encompassed by the amended claims are not anticipated by Sidler *et al.*

In view of these amendments and remarks, it is submitted that the rejection under 35 U.S.C. § 102(b) should be withdrawn and not applied to the newly submitted claims.

The Rejection of the Claims Under 35 U.S.C. § 103(a) Should Be Withdrawn

Claims 7, 9, 10, 13, 16, 17, 22, and 23 have been rejected under 35 U.S.C. § 103 as being unpatentable over Sidler *et al.* ((1998) *Plant Cell* 10:1623-1636) in view of Applicants' admission. Claims 4 and 18 have been amended. New claims 33-41 have been added. This rejection is respectfully traversed and should not be applied to the newly submitted claims.

The Office Action again indicates that Applicants admit that methods of transforming monocot plants and dicot plants were known in the art at the time of Applicants' invention and that in view of the teachings of Sidler *et al.* discussed *supra*, Applicants' invention would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention.

As discussed above, the Office Action asserts that the Sidler *et al.* reference discloses an isolated nucleotide sequence, *AtPGP1*, that would hybridize under the claimed stringency conditions to SEQ ID NO: 7 or 8. Also as discussed above, Applicants respectfully disagree with the position of the Office Action because, under the recited stringency conditions, the isolated nucleotide molecule disclosed in the the Sidler *et al.* reference would not hydridize to the nucleotide sequence set forth in either SEQ ID NO: 7 or 8. In the interest of furthering prosecution, claim 4, from which claims, 9, 10, 13, 16, and 17 depend, and claim 18, from which claims 22 and 23 depend, have been amended to recite that stringent conditions comprise hybridization at 37°C in 50% formamide, 1 M NaCl, and 1% SDS and a wash in 0.1X SSC at 60°C. Applicants submit that the isolated nucleotide molecule disclosed in the the Sidler *et al.*

reference would not hydridize to the nucleotide sequence set forth in either SEQ ID NO: 7 or 8 under the hybridization conditions recited in the amended claims. Thus, claims 7, 9, 10, 13, 16, 17, 22, and 23, particularly in view of this amendment, are not drawn to the isolated nucleotide molecule disclosed by Sidler *et al.*

Other than the assertion that the isolated nucleotide molecule disclosed by Sidler *et al.* would hybridize to SEQ ID NO: 7 or 8, the Office Action does not indicate that Sidler *et al.* teach, or render obvious, the nucleotide sequences set forth in SEQ ID NO: 7 or 8, those that encode the amino acid sequence set forth in SEQ ID NO: 9, and the fragments and variants set forth in parts (c) and (e)-(h) of claims 4 and 18. Thus, Sidler *et al.* neither teach nor render obvious an important aspect of Applicants' claimed invention, the isolated nucleotide molecules as claimed.

In view of these amendments and remarks, it is submitted that the rejections under 35 U.S.C. § 103 should be withdrawn and not applied to the newly submitted claims.

The Provisional Rejection of the Claims for Double Patenting Should Be Withdrawn

Claims 1-18 and 20-24 have been provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-18, 20-22, and 29 of copending Application No. 09/711,562. The Office Action indicates that Applicants did not specifically address this provisional rejection in their previous response to the Office. The Office Action mailed May 21, 2002 indicates that, although the conflicting claims are not identical, they are not patentably distinct from each other because both applications claim a nucleotide molecule that would inherently hybridize to each other under stringent conditions.

Additionally, Applicants note that this provisional rejection of the claims is now moot because Application No. 09/711,562 has become abandoned. A Notice of Abandonment of Application No. 09/711,562 was mailed on August 15, 2002.

Applicants, however, submit concurrently herewith a Supplemental Information Disclosure Statement and Form 1449 with one citation. The citation is to Publication No. US2002-016214-A1, which corresponds to copending Application No. 10/101,388, filed on March 19, 2002, which is a continuation of Application No. 09/711,562.

Should the Examiner maintain the rejection in view of Application No. 10/101,388, upon notification of allowable subject matter, Applicants will either timely file a terminal disclaimer compliant with 37 CFR 1.130(b) or demonstrate that the presently claimed subject matter is patentably distinct from the claimed invention of Application No. 10/101,388.

In view of the remarks and the abandonment of Application No. 09/711,562, it is submitted that the provisional rejection of the claims under the judicially created doctrine of obviousness-type double patenting should be withdrawn and held until such time that the claims are deemed allowable.

CONCLUSIONS

In view of the above amendments and remarks, Applicants submit that the rejections of the claims under 35 U.S.C. §§ 102, 103, and 112, and the provisional rejections of the claims under the judicially created doctrine of obviousness-type double patenting are overcome. Applicants respectfully submit that this application is now in condition for allowance. Early notice to this effect is solicited.

If in the opinion of the Examiner a telephone conference would expedite the prosecution of the subject application, the Examiner is invited to call the undersigned.

It is not believed that extensions of time or fees for net addition of claims are required, beyond those that may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 C.F.R. § 1.136(a), and any fee

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required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-0605.

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Marilyn Muñoz

Version with Markings to Show Changes Made:

In The Claims:

Please amend claims 1, 4, 18, and 24 as follows:

1. (Twice Amended) An isolated nucleotide molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence set forth in SEQ ID NO: 7;

(b) a nucleotide sequence set forth in SEQ ID NO: 8;

(c) a nucleotide sequence consisting of at least 19 contiguous nucleotides of the nucleotide sequence set forth in (b);

(d) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 9;

(e) a nucleotide sequence encoding at least 70 contiguous amino acids of the amino acid sequence set forth in SEQ ID NO: 9;

(f) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 7;

(g) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 8;

(h) a nucleotide sequence that is complementary to a nucleotide sequence selected from the group consisting of the nucleotide sequences set forth in (a)-(g); and

(i) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence selected from the group consisting of the nucleotide sequences set forth in (a) and (b) and complementary sequences thereof, said stringent conditions comprising hybridization at 37°C in [45%] 50% formamide, 1 M NaCl, and 1% SDS and a wash in [1X] 0.1X SSC at [55°C;] 60°C;

wherein said nucleotide molecule encodes a P-glycoprotein that controls plant growth or said nucleotide molecule is complementary to a nucleotide sequence that encodes said P-glycoprotein.

4. (Twice Amended) A transformed plant having stably incorporated into its genome a nucleotide molecule operably linked to a promoter that drives expression in a plant cell, wherein said nucleotide molecule comprises a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence set forth in SEQ ID NO: 7;

(b) a nucleotide sequence set forth in SEQ ID NO: 8;

(c) a nucleotide sequence consisting of at least 19 contiguous nucleotides of the nucleotide sequence set forth in (b);

(d) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 9;

(e) a nucleotide sequence encoding at least 70 contiguous amino acids of the amino acid sequence set forth in SEQ ID NO: 9;

(f) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 7;

(g) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 8;

(h) a nucleotide sequence that is complementary to a nucleotide sequence selected from the group consisting of the nucleotide sequences set forth in (a)-(g); and

(i) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence selected from the group consisting of the nucleotide sequences set forth in (a) and (b) and complementary sequences thereof, said stringent conditions comprising hybridization at 37°C in [45%] 50% formamide, 1 M NaCl, and 1% SDS and a wash in [1X] 0.1X SSC at [55°C;] 60°C;

wherein said nucleotide molecule encodes a P-glycoprotein that controls plant growth or said nucleotide molecule is complementary to a nucleotide sequence that encodes said P-glycoprotein.

18. (Twice Amended) A method for modifying the growth of a plant, said method comprising a plant with a nucleotide molecule encoding a P-glycoprotein wherein said P-glycoprotein functions to control growth of a plant, said nucleotide molecule operably linked to a promoter that drives expression of said nucleotide molecule in said plant, said nucleotide molecule comprises a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence set forth in SEQ ID NO: 7;

(b) a nucleotide sequence set forth in SEQ ID NO: 8;

(c) a nucleotide sequence consisting of at least 19 contiguous nucleotides of the nucleotide sequence set forth in (b);

(d) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 9;

(e) a nucleotide sequence encoding at least 70 contiguous amino acids of the amino acid sequence set forth in SEQ ID NO: 9;

(f) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 7;

(g) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 8;

(h) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a)-(g); and

(i) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence selected from the group consisting of the nucleotide sequences set forth in (a) and (b) and complementary sequences thereof, said stringent conditions comprising hybridization at 37°C in [45%] 50% formamide, 1 M NaCl, and 1% SDS and a wash in [1X] 0.1X SSC at [55°C;] 60°C;

wherein the growth of said transformed plant is modified.

24. (Twice Amended) A transformed plant cell having stably incorporated into its genome a nucleotide molecule operably linked to a promoter that drives expression in a plant cell, wherein said nucleotide molecule comprises a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence set forth in SEQ ID NO: 7;

(b) a nucleotide sequence set forth in SEQ ID NO: 8;

(c) a nucleotide sequence consisting of at least 19 contiguous nucleotides of the nucleotide sequence set forth in (b);

(d) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 9;

(e) a nucleotide sequence encoding at least 70 contiguous amino acids of the amino acid sequence set forth in SEQ ID NO: 9;

(f) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 7;

(g) a nucleotide sequence comprising at least 80% identity to the sequence set forth in SEQ ID NO: 8;

(h) a nucleotide sequence that is complementary to a nucleotide sequence selected from the group consisting of the nucleotide sequences set forth in (a)-(g); and

(i) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence selected from the group consisting of the nucleotide sequences set forth in (a) and (b) and complementary sequences thereof, said stringent conditions comprising hybridization at 37°C in [45%] 50% formamide, 1 M NaCl, and 1% SDS and a wash in [1X] 0.1X SSC at [55°C;] 60°C;

wherein said nucleotide molecule encodes a P-glycoprotein that controls plant growth or said nucleotide molecule is complementary to a nucleotide sequence that encodes said P-glycoprotein.